

Patent Application US/07/666,252

1 **SEQUENCE LISTING**

**(1) GENERAL INFORMATION:**

(i) APPLICANT: WAHL, DR, GEOFFREY M  
O'GORMAN DR, STEPHEN V

(ii) TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL THEREFOR

(iii) NUMBER OF SEQUENCES: 2

**(iv) CORRESPONDENCE ADDRESS:**

(A) ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY  
(B) STREET: 135 South LaSalle Street, Suite 900  
(C) CITY: Chicago  
(D) STATE: Illinois  
(E) COUNTRY: USA  
(F) ZIP: 60603

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/666,252  
(B) FILING DATE: 08-MAR-1991  
(C) CLASSIFICATION:

**(viii) ATTORNEY/AGENT INFORMATION:**

(A) NAME: REITER MR, STEPHEN E  
(B) REGISTRATION NUMBER: 31192  
(C) REFERENCE/DOCKET NUMBER: 50730

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (619) 552-1311  
(B) TELEFAX: (619) 552-0095  
(C) TELEX: 20 6566 PATLAW CGO

(2) INFORMATION FOR SEQ ID NO:1:

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 1380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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56 (vii) IMMEDIATE SOURCE:  
57 (B) CLONE: NATIVE FLP  
58  
59 (ix) FEATURE:  
60 (A) NAME/KEY: CDS  
61 (B) LOCATION: 1..1269  
62  
63  
64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
65  
66 ATG CCA CAA TTT GAT ATA TTA TGT AAA ACA CCA CCT AAG GTG CTT GTT 48  
67 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val  
68 1 5 10 15  
69  
70 CGT CAG TTT GTG GAA AGG TTT GAA AGA CCT TCA GGT GAG AAA ATA GCA 96  
71 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala  
72 20 25 30  
73  
74 TTA TGT GCT GAA CTA ACC TAT TTA TGT TGG ATG ATT ACA CAT AAC 144  
75 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn  
76 35 40 45  
77  
78 GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AAT ACT ATC ATA 192  
79 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile  
80 50 55 60  
81  
82 AGC AAT TCG CTG AGT TTC GAT ATT GTC AAT AAA TCA CTC CAG TTT AAA 240  
83 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys  
84 65 70 75 80  
85  
86 TAC AAG ACG CAA AAA GCA ACA ATT CTG GAA GCC TCA TTA AAG AAA TTG 288  
87 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu  
88 85 90 95  
89  
90 ATT CCT GCT TGG GAA TTT ACA ATT ATT CCT TAC TAT GGA CAA AAA CAT 336  
91 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His  
92 100 105 110  
93  
94 CAA TCT GAT ATC ACT GAT ATT GTA AGT AGT TTG CAA TTA CAG TTC GAA 384  
95 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu  
96 115 120 125  
97  
98 TCA TCG GAA GAA GCA GAT AAG GGA AAT AGC CAC AGT AAA AAA ATG CTT 432  
99 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu  
100 130 135 140  
101  
102 AAA GCA CTT CTA AGT GAG GGT GAA AGC ATC TGG GAG ATC ACT GAG AAA 480  
103 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys  
104 145 150 155 160  
105  
106 ATA CTA AAT TCG TTT GAG TAT ACT TCG AGA TTT ACA AAA ACA AAA ACT 528

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107	Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr			
108	165	170	175	
109				
110	TTA TAC CAA TTC CTC CTA GCT ACT TTC ATC AAT TGT GGA AGA TTC	576		
111	Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe			
112	180	185	190	
113				
114	AGC GAT ATT AAG AAC GTT GAT CCG AAA TCA TTT AAA TTA GTC CAA AAT	624		
115	Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn			
116	195	200	205	
117				
118	AAG TAT CTG GGA GTA ATA ATC CAG TGT TTA GTG ACA GAG ACA AAG ACA	672		
119	Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr			
120	210	215	220	
121				
122	AGC GTT AGT AGG CAC ATA TAC TTC TTT AGC GCA AGG GGT AGG ATC GAT	720		
123	Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp			
124	225	230	235	240
125				
126	CCA CTT GTA TAT TTG GAT GAA TTT TTG AGG AAT TCT GAA CCA GTC CTA	768		
127	Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu			
128	245	250	255	
129				
130	AAA CGA GTA AAT AGG ACC GGC AAT TCT TCA AGC AAT AAA CAG GAA TAC	816		
131	Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Asn Lys Gln Glu Tyr			
132	260	265	270	
133				
134	CAA TTA TTA AAA GAT AAC TTA GTC AGA TCG TAC AAT AAA GCT TTG AAG	864		
135	Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys			
136	275	280	285	
137				
138	AAA AAT GCG CCT TAT TCA ATC TTT GCT ATA AAA AAT GGC CCA AAA TCT	912		
139	Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser			
140	290	295	300	
141				
142	CAC ATT GGA AGA CAT TTG ATG ACC TCA TTT CTT TCA ATG AAG GGC CTA	960		
143	His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu			
144	305	310	315	320
145				
146	ACG GAG TTG ACT AAT GTT GTG GGA AAT TGG AGC GAT AAG CGT GCT TCT	1008		
147	Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser			
148	325	330	335	
149				
150	GCC GTG GCC AGG ACA ACG TAT ACT CAT CAG ATA ACA GCA ATA CCT GAT	1056		
151	Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp			
152	340	345	350	
153				
154	CAC TAC TTC GCA CTA GTT TCT CGG TAC TAT GCA TAT GAT CCA ATA TCA	1104		
155	His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser			
156	355	360	365	
157				
158	AAG GAA ATG ATA GCA TTG AAG GAT GAG ACT AAT CCA ATT GAG GAG TGG	1152		
159	Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp			

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160 370 375 380  
161  
162 CAG CAT ATA GAA CAG CTA AAG GGT AGT GCT GAA GGA AGC ATA CGA TAC 1200  
163 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr  
164 385 390 395 400  
165  
166 CCC GCA TGG AAT GGG ATA ATA TCA CAG GAG GTA CTA GAC TAC CTT TCA 1248  
167 Pro Ala Trp Asn Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser  
168 405 410 415  
169  
170 TCC TAC ATA AAT AGA CGC ATA TAAGTACGCA TTTAAGCATA AACACGCACT 1299  
171 Ser Tyr Ile Asn Arg Arg Ile  
172 420  
173  
174 ATGCCGTTCT TCTCATGTAT ATATATATAC AGGCAACACG CAGATATAGG TGCGACGTGA 1359  
175  
176 ACAGTGAGCT GTATGTGCGC A 1380  
177  
178  
179 (2) INFORMATION FOR SEQ ID NO:2:  
180  
181 (i) SEQUENCE CHARACTERISTICS:  
182 (A) LENGTH: 423 amino acids  
183 (B) TYPE: amino acid  
184 (D) TOPOLOGY: linear  
185  
186 (ii) MOLECULE TYPE: protein  
187  
188 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
189  
190 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val  
191 1 5 10 15  
192  
193 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala  
194 20 25 30  
195  
196 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn  
197 35 40 45  
198  
199 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile  
200 50 55 60  
201  
202 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys  
203 65 70 75 80  
204  
205 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu  
206 85 90 95  
207  
208 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His  
209 100 105 110  
210  
211 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu  
212 115 120 125

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213  
214 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu  
215 130 135 140  
216  
217 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys  
218 145 150 155 160  
219  
220 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr  
221 165 170 175  
222  
223 Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe  
224 180 185 190  
225  
226 Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn  
227 195 200 205  
228  
229 Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr  
230 210 215 220  
231  
232 Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp  
233 225 230 235 240  
234  
235 Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu  
236 245 250 255  
237  
238 Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr  
239 260 265 270  
240  
241 Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys  
242 275 280 285  
243  
244 Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser  
245 290 295 300  
246  
247 His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu  
248 305 310 315 320  
249  
250 Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser  
251 325 330 335  
252  
253 Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp  
254 340 345 350  
255  
256 His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser  
257 355 360 365  
258  
259 Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp  
260 370 375 380  
261  
262 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr  
263 385 390 395 400  
264  
265 Pro Ala Trp Asn Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser

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266

405

410

415

267

268 Ser Tyr Ile Asn Arg Arg Ile

269 420

270

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SEQUENCE VERIFICATION REPORT  
PATENT APPLICATION US/07/666,252

DATE: 04/26/91

TIME: 13:03:31

LINE ERROR

ORIGINAL TEXT

30 Wrong application Serial Number  
31 Wrong Filing Date

Off (A) APPLICATION NUMBER: US 07/666,252  
(B) FILING DATE: 08-MAR-1991

PAGE: 1

SEQUENCE MISSING ITEM REPORT  
PATENT APPLICATION US/07/666,252

DATE: 04/26/91  
TIME: 13:03:31

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA  
APPLICATION NUMBER  
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT  
PATENT APPLICATION US/07/666,252

DATE: 04/26/91  
TIME: 13:03:31

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CORRECTED TEXT